

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/539,213  
Source: PG/10  
Date Processed by STIC: 6/24/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 06/24/2005

PATENT APPLICATION: US/10/539,213

TIME: 15:21:15

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\06242005\J539213.raw

3 <110> APPLICANT: Agrinomics LLC  
 5 <120> TITLE OF INVENTION: GENERATION OF PLANTS WITH ALTERED OIL CONTENT  
 7 <130> FILE REFERENCE: 6616-71292-08  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,213  
 C--> 9 <141> CURRENT FILING DATE: 2005-06-17  
 9 <150> PRIOR APPLICATION NUMBER: PCT/US2003/041146  
 10 <151> PRIOR FILING DATE: 2003-12-18  
 12 <150> PRIOR APPLICATION NUMBER: 60/434,763  
 13 <151> PRIOR FILING DATE: 2002-12-18  
 15 <160> NUMBER OF SEQ ID NOS: 6  
 17 <170> SOFTWARE: PatentIn version 3.2  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 5034  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Arabidopsis thaliana  
 24 <400> SEQUENCE: 1

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27	aggcctgaac	aatcttttga	atccccgcct	tttcgatgga	gggattcgcc	ttcttctcac	120
29	catgttcctc	gagagttttc	ttctcgtttg	ggatctggag	acttccgcag	accttcttca	180
31	ttaacacagc	tcttaagatt	gataggaagt	gaattgatga	ggttactctt	caaaggagca	240
33	atttttaata	ctcaggggtg	acggcaccag	tttgtggagg	agactagtca	tggatacaca	300
35	tcttctcggg	ccagtgcgcc	aatgtttgat	aattatagga	catcagcatc	gcgtggagac	360
37	tggagatata	ccaggaattg	cagggatgat	agagtttctg	taagccaaaa	ggaatggaaa	420
39	tgcaatacat	gggagatgag	caacggatct	tctagaagtt	ttgagaggcc	atttggattt	480
41	agaaatggtc	ggaggtcagt	tgatgaaagg	ccgctacatg	cttcagatac	tcattctacc	540
43	gtggtgaact	ctttggatcc	agccaactcg	gctcattatc	tggacaatga	gatcagttac	600
45	ccagtacggg	ctcttaaaat	taaaaatgag	cataaatttt	cagatcaaag	gttatcactt	660
47	ccttcagatc	ctcattctga	atgtattagc	ttgtttgaac	ggccttcttc	tgagaacaat	720
49	tatggcaata	aggtttggtc	accagcaaag	caatgcaatg	atttgatgta	tggtcgaagg	780
51	ttagttagtg	ataattcatt	agatgctcca	atccccaatg	cagagctgga	ggggacttgg	840
53	gaacaacttc	gcctgaaaga	cccgcagat	aacaatagtt	tacatggtat	caatgatata	900
55	gacggtgata	ggaaatgtgc	aaaggagagt	tctctgggag	caactgggaa	acttccactg	960
57	tggaatagtt	ctgggagttt	tgcattctcag	agttcagggt	ttagtcattc	aagtagcttg	1020
59	aaaagcttgg	gggctgttga	ttccagcgat	cggagagattg	aggttcttcc	taaaattggt	1080
61	actgtgactc	aatcttcttc	aggagacgct	actgcctgtg	ccacaactac	tcattcttct	1140
63	gaggagatga	gttctagaaa	gaaacaacgt	ctcgggtggg	gtgaggggact	ggcgaatat	1200
65	gagaaaaaga	aagttgatgt	taacccaaat	gaagatggaa	caacattgat	ggaaaacggt	1260
67	ttagaggaac	tacattcggt	aaacaaaaat	attgctgata	aaagtcccac	agcagccatt	1320
69	gttccagatt	atggttcccc	tacaacacca	tcctctgtag	cttgcagttc	atcaccaggg	1380
71	tttgctgata	aatcatctcc	gaaggctgct	atagctgcta	gtgatgtcag	taacatgtgc	1440
73	cgttcgccct	gtcccggtgc	tagtattcac	cttgaacgat	tcccaatcaa	tatcgaggag	1500
75	ctcgataaca	tctcaatgga	gcgttttggc	tgtttactca	atgagttact	tggtagtgat	1560
77	gattctggta	caggggattc	cagttctgtc	caattgacat	caatgaacac	attacttgcc	1620

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81	aacaaacata	ggacactaaa	gcttgaaggt	agaagacact	ctcgtgttgt	tggacccagt	1740
83	tcatactgtt	gtgatggaga	tgcaaagtgt	cccaaggagc	aggcttcttg	tagtttggt	1800
85	cctaaggcaa	cagcttcttc	tgtagctaaa	acactgggtga	gagctcctgt	gcatcaggct	1860
87	ggtttagcca	aggttcctgc	tgatgttttt	gaagatagtc	ctgggggaagt	taaacctcta	1920
89	tcccaatctt	ttgccactgt	tgaaagagag	gaagatatac	tgcccataacc	atctatgaag	1980
91	gcagctgttt	cttcgaaaga	gattaacaca	cctgcttttg	ccaatcagga	aactattgag	2040
93	gtttcttctg	ctgatgacag	catggcctcc	aaagaagact	tgttctgggc	taagttatta	2100
95	tctgccaata	agaaatatgc	ttgtgaatca	tctggagtat	tcaatcaatt	gcttccaaga	2160
97	gattttaatt	cgtctgacaa	ctcaagattc	cctggcatat	gtcaaacgca	gtttgattct	2220
99	catgtccaag	aaaaaattgc	agatagggtg	ggcctattga	gagctaggga	gaaaatttta	2280
101	ctccttcagt	ttaaagcggt	tcagctctca	tggaaagaa	atttggatca	gctagcttta	2340
103	gcaaagtacc	aatcaaagtc	tagcaaaaaa	acagaactat	atccgaatgc	aaaaaatgga	2400
105	gggtatctga	agcttcccca	atctgtacgc	ctgaggttct	cttcttcagc	tccaagaagg	2460
107	gatagtgtag	tccccacaac	agagctcgta	agttatatgg	aaaagctact	tccgggtacc	2520
109	catctaaagc	cttttagaga	cattttgaaa	atgcctgcta	tgattttgga	tgagaaagag	2580
111	aggggtgatgt	cgaggtttat	ttctagcaat	ggactgattg	aagatccatg	tgacgttgag	2640
113	aaggaaagaa	caatgattaa	tccttggaac	tcagaggaga	aagaaatctt	tctgaatttg	2700
115	ctagcaatgc	atgggaagga	tttcaagaag	attgcttcat	ctcttaccga	aaagacaact	2760
117	gcggaactgta	ttgattacta	ctacaaaaac	cacaagtctg	attgttttgg	gaaaataaag	2820
119	aagcagcgtg	cttatggtaa	ggaagggaag	cacacctaca	tgttggctcc	acgaaaaaag	2880
121	tggaaacgtg	agatgggggc	tgccctctct	gatattttag	gggatgtctc	cattatagca	2940
123	gcaaacgctg	gaaaggttgc	atcaaccagg	ccgatctctt	ccaaaaagat	cacccttaga	3000
125	ggttgacagca	gtgctaattc	attgcagcac	gatggaaata	actctgaagg	gtgctcctac	3060
127	agttttgatt	tcccacgtaa	gagaactgct	ggtgcagatg	ttttagctgt	tggtcctttg	3120
129	tcaccagagc	agataaattc	ttgcttaagg	acttctgtga	gctctagaga	gagggtgatg	3180
131	gatcatctga	agtttaatac	tgctgtaaa	aaacctcgga	tatctcatac	tctacataat	3240
133	gagaacagca	atactctaca	caatgagaac	agcaacgaag	aagatgactc	atgttcggaa	3300
135	gagagctgtg	gggaaacagg	tcctattcac	tggacagatg	atgagagatc	tgccctttata	3360
137	cagggttttt	cgcttttttg	caagaatttt	gcttcaatat	caaggtagct	cgggacaaga	3420
139	tctccagatc	agtgtaaagg	tttcttcagc	aaagttcgga	aatgtcttgg	gttggaatct	3480
141	ataaagtttg	gatctggaaa	tgtaagcaca	tccgtaagtg	ttgataatgg	caatgagggt	3540
143	ggtgggagcg	acttggaaga	tccttgtcct	atggagagta	actctggcat	agtgaataat	3600
145	ggagtttggt	ccaagatggg	tatgaattct	cctacctcac	cttttaatat	gaatcaggat	3660
147	ggtgttaatc	aatcaggctc	tgcaaatgtg	aaagccgacc	ttagtagatc	agaagaagag	3720
149	aatgggcaga	aatattttgt	tctgaaagat	gataataatc	tcgtgaacaa	tgcatatgtc	3780
151	aatggcggtt	tcccgagtct	agtttcagaa	tcttgtagag	atttggtaga	tattaatact	3840
153	gttgagagcc	agtctcaggc	tgccggaaaa	agcaagagca	atgatctcat	gtcaatggaa	3900
155	atcgatgaag	gtgtcttaac	atctgtcact	atatcttccg	agccattgta	ttgtggccta	3960
157	agtgttcttt	ccaatgttat	tgtggaaacc	cctacagaaa	tctcacgaaa	gggctcagga	4020
159	gatcaagggt	ctacaatgcc	ttaaatttagt	tcaaagaatc	aagatggagt	gatgcaagct	4080
161	gcaaacagaa	ccagaaattc	tggccttgaa	cctgaaagtg	caccttcagg	tttcagggtac	4140
163	cctgagtgtc	ttcaccatgt	tccgatttag	gtgtgtacgg	aaaaccctat	aggcgtcagt	4200
165	gcaccacgag	gaaatccaaa	ttgccatgca	gagtcagagt	caggaaattc	tcttgttgga	4260
167	caagttgacg	aaacacatga	cttgggttgg	cccaagaaca	atctgggaatt	ggatgggagg	4320
169	cttcagggtt	taggccatgt	aaaccctgag	cagatttggtc	tactaaaagc	gaccaataca	4380
171	gaatcttgtc	aaaatcccca	gagatcagtc	acccaagatc	tgagcaggat	aagtagatca	4440
173	aaatctgatt	tgatcgtaaa	aacccaacgt	acaggtgaag	gcttctcact	caccaagtgt	4500
175	actagttcag	ctcctaagcc	tctggcagta	tcccataaag	agggcagatc	tggtcatagc	4560

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177 aggagccatt cgtttagttt gtctgatact gagagactcc acaagaatgg agatgtgaaa 4620
179 ctgtttggtta cagtacttac tactgatgag aatggaataa aacaaaaaca caatccatgt 4680
181 ggaattgtca ggcatcatc aaccttgagc agggaccatg atacaagaca tcattacatt 4740
183 aatcagcaac accttcagaa cgttcccatc acgagctacg gtttttgga tggcaacaga 4800
185 attcaaaccg ggctcacatc tttgccagag tcggccaagt tgcttgcaag ttgccctgaa 4860
187 gcattttcca cgcactaaa gcagcaagtt ggtaacagca aagagattct ggtggatgtt 4920
189 aatggtggaa ttttgagctt tggttaagcat aacgaagata gagctgagtc ctcaagcgct 4980
191 aaggatgaag gtaacatagg aggggtaaatt ggtgtagcag aggcagccac gtga 5034
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 1677
196 <212> TYPE: PRT
197 <213> ORGANISM: Arabidopsis thaliana
199 <400> SEQUENCE: 2
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202 1 5 10 15
205 Arg Lys His Asp Arg Pro Glu Gln Ser Phe Glu Ser Pro Pro Phe Arg
206 20 25 30
209 Trp Arg Asp Ser Pro Ser Ser His His Val Pro Arg Glu Phe Ser Ser
210 35 40 45
213 Arg Leu Gly Ser Gly Asp Phe Arg Arg Pro Ser Ser Leu Thr Gln Leu
214 50 55 60
217 Leu Arg Leu Ile Gly Ser Glu Leu Met Arg Leu Leu Phe Lys Gly Ala
218 65 70 75 80
221 Ile Phe Asn Thr Gln Gly Gly Arg His Gln Phe Val Glu Glu Thr Ser
222 85 90 95
225 His Gly Tyr Thr Ser Ser Arg Ser Ser Ala Arg Met Phe Asp Asn Tyr
226 100 105 110
229 Arg Pro Ser Ala Ser Arg Gly Asp Trp Arg Tyr Thr Arg Asn Cys Arg
230 115 120 125
233 Asp Asp Arg Val Ser Val Ser Gln Lys Glu Trp Lys Cys Asn Thr Trp
234 130 135 140
237 Glu Met Ser Asn Gly Ser Ser Arg Ser Phe Glu Arg Pro Phe Gly Ile
238 145 150 155 160
241 Arg Asn Gly Arg Arg Ser Val Asp Glu Arg Pro Leu His Ala Ser Asp
242 165 170 175
245 Thr His Ser Thr Val Val Asn Ser Leu Asp Pro Ala Asn Ser Ala His
246 180 185 190
249 Tyr Leu Asp Asn Glu Ile Ser Thr Pro Val Arg Ser Leu Lys Ile Lys
250 195 200 205
253 Asn Glu His Lys Phe Ser Asp Gln Arg Leu Ser Leu Pro Ser Asp Pro
254 210 215 220
257 His Ser Glu Cys Ile Ser Leu Phe Glu Arg Pro Ser Ser Glu Asn Asn
258 225 230 235 240
261 Tyr Gly Asn Lys Val Cys Ser Pro Ala Lys Gln Cys Asn Asp Leu Met
262 245 250 255
265 Tyr Gly Arg Arg Leu Val Ser Asp Asn Ser Leu Asp Ala Pro Ile Pro
266 260 265 270
269 Asn Ala Glu Leu Glu Gly Thr Trp Glu Gln Leu Arg Leu Lys Asp Pro
270 275 280 285

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273 Gln Asp Asn Asn Ser Leu His Gly Ile Asn Asp Ile Asp Gly Asp Arg
274      290      295      300
277 Lys Cys Ala Lys Glu Ser Ser Leu Gly Ala Thr Gly Lys Leu Pro Leu
278 305      310      315      320
281 Trp Asn Ser Ser Gly Ser Phe Ala Ser Gln Ser Ser Gly Phe Ser His
282      325      330      335
285 Ser Ser Ser Leu Lys Ser Leu Gly Ala Val Asp Ser Ser Asp Arg Lys
286      340      345      350
289 Ile Glu Val Leu Pro Lys Ile Val Thr Val Thr Gln Ser Ser Ser Gly
290      355      360      365
293 Asp Ala Thr Ala Cys Ala Thr Thr Thr His Leu Ser Glu Glu Met Ser
294      370      375      380
297 Ser Arg Lys Lys Gln Arg Leu Gly Trp Gly Glu Gly Leu Ala Lys Tyr
298 385      390      395      400
301 Glu Lys Lys Lys Val Asp Val Asn Pro Asn Glu Asp Gly Thr Thr Leu
302      405      410      415
305 Met Glu Asn Gly Leu Glu Glu Leu His Ser Leu Asn Lys Asn Ile Ala
306      420      425      430
309 Asp Lys Ser Pro Thr Ala Ala Ile Val Pro Asp Tyr Gly Ser Pro Thr
310      435      440      445
313 Thr Pro Ser Ser Val Ala Cys Ser Ser Ser Pro Gly Phe Ala Asp Lys
314      450      455      460
317 Ser Ser Pro Lys Ala Ala Ile Ala Ala Ser Asp Val Ser Asn Met Cys
318 465      470      475      480
321 Arg Ser Pro Ser Pro Val Ser Ser Ile His Leu Glu Arg Phe Pro Ile
322      485      490      495
325 Asn Ile Glu Glu Leu Asp Asn Ile Ser Met Glu Arg Phe Gly Cys Leu
326      500      505      510
329 Leu Asn Glu Leu Leu Gly Thr Asp Asp Ser Gly Thr Gly Asp Ser Ser
330      515      520      525
333 Ser Val Gln Leu Thr Ser Met Asn Thr Leu Leu Ala Trp Lys Gly Glu
334      530      535      540
337 Ile Leu Lys Ala Val Glu Met Thr Glu Ser Glu Ile Asp Leu Leu Glu
338 545      550      555      560
341 Asn Lys His Arg Thr Leu Lys Leu Glu Gly Arg Arg His Ser Arg Val
342      565      570      575
345 Val Gly Pro Ser Ser Tyr Cys Cys Asp Gly Asp Ala Asn Val Pro Lys
346      580      585      590
349 Glu Gln Ala Ser Cys Ser Leu Asp Pro Lys Ala Thr Ala Ser Ser Val
350      595      600      605
353 Ala Lys Thr Leu Val Arg Ala Pro Val His Gln Ala Gly Leu Ala Lys
354      610      615      620
357 Val Pro Ala Asp Val Phe Glu Asp Ser Pro Gly Glu Val Lys Pro Leu
358 625      630      635      640
361 Ser Gln Ser Phe Ala Thr Val Glu Arg Glu Glu Asp Ile Leu Pro Ile
362      645      650      655
365 Pro Ser Met Lys Ala Ala Val Ser Ser Lys Glu Ile Asn Thr Pro Ala
366      660      665      670
369 Phe Ala Asn Gln Glu Thr Ile Glu Val Ser Ser Ala Asp Asp Ser Met

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370          675          680          685
373 Ala Ser Lys Glu Asp Leu Phe Trp Ala Lys Leu Leu Ser Ala Asn Lys
374          690          695          700
377 Lys Tyr Ala Cys Glu Ser Ser Gly Val Phe Asn Gln Leu Leu Pro Arg
378 705          710          715          720
381 Asp Phe Asn Ser Ser Asp Asn Ser Arg Phe Pro Gly Ile Cys Gln Thr
382          725          730          735
385 Gln Phe Asp Ser His Val Gln Glu Lys Ile Ala Asp Arg Val Gly Leu
386          740          745          750
389 Leu Arg Ala Arg Glu Lys Ile Leu Leu Leu Gln Phe Lys Ala Phe Gln
390          755          760          765
393 Leu Ser Trp Lys Lys Asp Leu Asp Gln Leu Ala Leu Ala Lys Tyr Gln
394          770          775          780
397 Ser Lys Ser Ser Lys Lys Thr Glu Leu Tyr Pro Asn Ala Lys Asn Gly
398 785          790          795          800
401 Gly Tyr Leu Lys Leu Pro Gln Ser Val Arg Leu Arg Phe Ser Ser Ser
402          805          810          815
405 Ala Pro Arg Arg Asp Ser Val Val Pro Thr Thr Glu Leu Val Ser Tyr
406          820          825          830
409 Met Glu Lys Leu Leu Pro Gly Thr His Leu Lys Pro Phe Arg Asp Ile
410          835          840          845
413 Leu Lys Met Pro Ala Met Ile Leu Asp Glu Lys Glu Arg Val Met Ser
414          850          855          860
417 Arg Phe Ile Ser Ser Asn Gly Leu Ile Glu Asp Pro Cys Asp Val Glu
418 865          870          875          880
421 Lys Glu Arg Thr Met Ile Asn Pro Trp Thr Ser Glu Glu Lys Glu Ile
422          885          890          895
425 Phe Leu Asn Leu Leu Ala Met His Gly Lys Asp Phe Lys Lys Ile Ala
426          900          905          910
429 Ser Ser Leu Thr Gln Lys Thr Thr Ala Asp Cys Ile Asp Tyr Tyr Tyr
430          915          920          925
433 Lys Asn His Lys Ser Asp Cys Phe Gly Lys Ile Lys Lys Gln Arg Ala
434          930          935          940
437 Tyr Gly Lys Glu Gly Lys His Thr Tyr Met Leu Ala Pro Arg Lys Lys
438 945          950          955          960
441 Trp Lys Arg Glu Met Gly Ala Ala Ser Leu Asp Ile Leu Gly Asp Val
442          965          970          975
445 Ser Ile Ile Ala Ala Asn Ala Gly Lys Val Ala Ser Thr Arg Pro Ile
446          980          985          990
449 Ser Ser Lys Lys Ile Thr Leu Arg Gly Cys Ser Ser Ala Asn Ser Leu
450          995          1000          1005
453 Gln His Asp Gly Asn Asn Ser Glu Gly Cys Ser Tyr Ser Phe Asp
454          1010          1015          1020
457 Phe Pro Arg Lys Arg Thr Ala Gly Ala Asp Val Leu Ala Val Gly
458          1025          1030          1035
461 Pro Leu Ser Pro Glu Gln Ile Asn Ser Cys Leu Arg Thr Ser Val
462          1040          1045          1050
465 Ser Ser Arg Glu Arg Cys Met Asp His Leu Lys Phe Asn His Val
466          1055          1060          1065

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 661,662,663,664,665,1186

**VERIFICATION SUMMARY**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660

M:341 Repeated in SeqNo=5